

RAW SEQUENCE LISTING

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Application Serial Number: 10/538,985
Source: PCT
Date Processed by STIC: 11/08/2005

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PCT

RAW SEQUENCE LISTING

DATE: 11/08/2005

PATENT APPLICATION: US/10/538,985

TIME: 12:19:08

Input Set : D:\voss008.txt

Output Set : N:\CRF4\11082005\J538985.raw

5 <110> APPLICANT: VILARDAGA, JEAN-PIERRE
6 HOFFMANN, CARSTEN
7 LOHSE, MARTIN, JOHANNES
10 <120> TITLE OF INVENTION: MILLISECOND ACTIVATION SWITCH FOR SEVEN-TRANSMEMBRANE
PROTEINS
12 <130> FILE REFERENCE: VOSS:008US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/538,985
15 <141> CURRENT FILING DATE: 2005-06-15
17 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/014679
18 <151> PRIOR FILING DATE: 2003-12-19
20 <150> PRIOR APPLICATION NUMBER: EP 03 00 4394.7
21 <151> PRIOR FILING DATE: 2003-03-03
23 <150> PRIOR APPLICATION NUMBER: DE 102 59 874.6
24 <151> PRIOR FILING DATE: 2002-12-19
26 <160> NUMBER OF SEQ ID NOS: 46
28 <170> SOFTWARE: PatentIn version 3.1
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34 <211> LENGTH: 1409
36 <212> TYPE: DNA
38 <213> ORGANISM: Mouse
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47 tccctgcagg tgacactgac gctgggtttgc ctggctggcc tgctcatgct gttcacagta 180
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61 ctcatctcca tagagaagaa gaccagaagt ggtatgtcat ctccctgtcc atcggttcct 600
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73 ccccgggggc ccgcagacc gaccgcggcc cccgagccaa gggcaagacc cgggcgagtc 960
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112 Gly Gly Thr Arg Ala Thr Pro Tyr Ser Leu Gln Val Thr Leu Thr Leu
113 35 40 45
116 Val Cys Leu Ala Gly Leu Leu Met Leu Phe Thr Val Phe Gly Asn Val
117 50 55 60
120 Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala Pro Gln
121 65 70 75 80
124 Asn Leu Phe Leu Val Ser Leu Ala Ser Ala Asp Ile Leu Val Ala Thr
125 85 90 95
128 Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr
129 100 105 110
132 Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe
133 115 120 125
136 Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr
137 130 135 140
140 Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro Arg
141 145 150 155 160
144 Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser Ala Val Ile
145 165 170 175
148 Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Ala Gly Gly Gly
149 180 185 190
152 Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp Gln Lys Trp Tyr
153 195 200 205
156 Val Ile Ser Ser Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met
157 210 215 220
160 Ile Leu Val Tyr Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg
161 225 230 235 240
164 Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Cys Ser Ala Pro Pro Gly
165 245 250 255
168 Gly Ala Asp Arg Arg Pro Asn Gly Leu Gly Pro Glu Arg Gly Ala Gly
169 260 265 270
172 Pro Thr Gly Ala Glu Ala Glu Pro Leu Pro Thr Gln Leu Asn Gly Ala
173 275 280 285
176 Pro Gly Glu Pro Ala Pro Ala Gly Pro Arg Asp Gly Asp Ala Leu Asp
177 290 295 300
180 Leu Glu Glu Ser Ser Ser Ser Glu His Ala Glu Arg Pro Pro Gly Pro
181 305 310 315 320
184 Arg Arg Pro Asp Arg Gly Pro Arg Ala Lys Gly Lys Thr Arg Ala Ser
185 325 330 335
188 Gln Val Lys Pro Gly Asp Ser Leu Pro Arg Arg Gly Pro Gly Ala Ala

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192 Gly Pro Gly Ala Ser Gly Ser Gly His Gly Glu Glu Arg Gly Gly Gly
193          355          360          365
196 Ala Lys Ala Ser Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe
197          370          375          380
200 Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Val Cys Trp Phe
201 385          390          395          400
204 Pro Phe Phe Phe Thr Tyr Thr Leu Ile Ala Val Gly Cys Pro Val Pro
205          405          410          415
208 Ser Gln Leu Phe Asn Phe Phe Phe Trp Phe Gly Tyr Cys Asn Ser Ser
209          420          425          430
212 Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His Asp Phe Arg Arg Ala
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222 <211> LENGTH: 1785
224 <212> TYPE: DNA
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235 ctgcaccgtg ctcaggccca gtgcgaaaaa cggctcaagg aggtcctgca gaggccagcc 180
237 agcataatgg aatcagacaa gggatggaca tctgcgtcca catcagggaa gcccaggaaa 240
239 gataaggcat ctgggaagct ctaccctgag tctgaggagg acaaggaggc acccactggc 300
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245 aaaggccatg cctaccgacg ctgtgaccgc aatggcagct gggagctggt gcctgggcac 480
247 aacaggacgt gggccaacta cagcgagtgt gtcaaatttc tcaccaatga gactcgtgaa 540
249 cgggagggtgt ttgaccgcct gggcatgatt tacaccgtgg gctactccgt gtccctggcg 600
251 tccctcaccg tagctgtgct catcctggcc tactttaggc ggctgcactg cacgcgcaac 660
253 tacatccaca tgcacctgtt cctgtccttc atgctgcgcg ccgtgagcat cttcgtcaag 720
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313 35 40 45
316 Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu
317 50 55 60
320 Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys
321 65 70 75 80
324 Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu
325 85 90 95
328 Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp
329 100 105 110
332 Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala
333 115 120 125
336 Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala
337 130 135 140
340 Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Leu Val Pro Gly His
341 145 150 155 160
344 Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn
345 165 170 175
348 Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr
349 180 185 190
352 Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile
353 195 200 205
356 Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met
357 210 215 220
360 His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys
361 225 230 235 240
364 Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu
365 245 250 255
368 Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala
369 260 265 270
372 Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe
373 275 280 285
376 Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu
377 290 295 300
380 Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr
381 305 310 315 320
384 Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val
385 325 330 335
388 Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp

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389          340          345          350
392 Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu
393          355          360          365
396 Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val
397          370          375          380
400 Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg
401 385          390          395          400
404 Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu
405          405          410          415
408 Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val
409          420          425          430
412 Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn
413          435          440          445
416 Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly
417          450          455          460
420 Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
421 465          470          475          480
424 Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
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440 Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
441 545          550          555          560
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VERIFICATION SUMMARY

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